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RAW SEQUENCE LISTING
PATENT APPLICATION: **US/09/870,353A**

DATE: 05/06/2003
TIME: 14:43:20

Input Set : **A:\-1-1-1.app**
Output Set: **N:\CRF4\05062003\I870353A.raw**

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 3 <110> APPLICANT: Wang, Yan
 4       Xi, Lei
 5       Prosen, Dennis E.
 6       MJ Bioworks, Inc.
 8 <120> TITLE OF INVENTION: Improved Nucleic Acid Modifying Enzymes
10 <130> FILE REFERENCE: 020130-000111US
12 <140> CURRENT APPLICATION NUMBER: US 09/870,353A
13 <141> CURRENT FILING DATE: 2001-05-30
15 <150> PRIOR APPLICATION NUMBER: US 60/207,567
16 <151> PRIOR FILING DATE: 2000-05-26
18 <150> PRIOR APPLICATION NUMBER: US 09/640,958
19 <151> PRIOR FILING DATE: 2000-08-16
21 <160> NUMBER OF SEQ ID NOS: 34
23 <170> SOFTWARE: PatentIn Ver. 2.1
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26 <211> LENGTH: 189
27 <212> TYPE: DNA
28 <213> ORGANISM: Artificial Sequence
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31 <223> OTHER INFORMATION: Description of Artificial Sequence:synthetic
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33       binding protein Ssod7d
35 <220> FEATURE:
36 <221> NAME/KEY: CDS
37 <222> LOCATION: (1)..(189)
38 <223> OTHER INFORMATION: Ssod7d
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43 ggccgtggtg cggtaagcga aaaggacgcg ccgaaggagc tgctgcagat gctggagaag 180
44 cagaaaaag                                                           189
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48 <211> LENGTH: 63
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53 <223> OTHER INFORMATION: Description of Artificial Sequence:synthetic
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55       binding protein Ssod7d
57 <400> SEQUENCE: 2
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60 Ser Lys Ile Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr
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71 <213> ORGANISM: Artificial Sequence
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77 <220> FEATURE:
78 <221> NAME/KEY: CDS
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85 gagggcggtg gcaagaccgg ccgtggtgcg gtaagcgaaa aggacgcgcc gaaggagctg 180
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114 ggccgcggcg gaggcgggca tcatcatcat catcattaa               1899
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Input Set : **A:\-1-1-1.app**
Output Set: **N:\CRF4\05062003\I870353A.raw**

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118 <211> LENGTH: 632
119 <212> TYPE: PRT
120 <213> ORGANISM: Artificial Sequence
122 <220> FEATURE:
123 <223> OTHER INFORMATION: Description of Artificial Sequence:fusion protein
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126 <400> SEQUENCE: 4
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128  1               5                  10                  15
129 Glu Lys Glu Val Asp Ile Ser Lys Ile Lys Lys Val Trp Arg Val Gly
130              20                  25                  30
131 Lys Met Ile Ser Phe Thr Tyr Asp Glu Gly Gly Gly Lys Thr Gly Arg
132          35                  40                  45
133 Gly Ala Val Ser Glu Lys Asp Ala Pro Lys Glu Leu Leu Gln Met Leu
134      50                  55                  60
135 Glu Lys Gln Lys Lys Gly Gly Gly Val Thr Ser Pro Lys Ala Leu Glu
136  65                  70                  75                  80
137 Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu
138              85                  90                  95
139 Ser Arg Lys Glu Pro Met Trp Ala Asp Leu Leu Ala Leu Ala Ala Ala
140          100                 105                 110
141 Arg Gly Gly Arg Val His Arg Ala Pro Glu Pro Tyr Lys Ala Leu Arg
142          115                 120                 125
143 Asp Leu Lys Glu Ala Arg Gly Leu Leu Ala Lys Asp Leu Ser Val Leu
144      130                 135                 140
145 Ala Leu Arg Glu Gly Leu Gly Leu Pro Pro Gly Asp Asp Pro Met Leu
146 145                 150                 155                 160
147 Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala
148              165                 170                 175
149 Arg Arg Tyr Gly Gly Glu Trp Thr Glu Glu Ala Gly Glu Arg Ala Ala
150          180                 185                 190
151 Leu Ser Glu Arg Leu Phe Ala Asn Leu Trp Gly Arg Leu Glu Gly Glu
152          195                 200                 205
153 Glu Arg Leu Leu Trp Leu Tyr Arg Glu Val Glu Arg Pro Leu Ser Ala
154      210                 215                 220
155 Val Leu Ala His Met Glu Ala Thr Gly Val Arg Leu Asp Val Ala Tyr
156 225                 230                 235                 240
157 Leu Arg Ala Leu Ser Leu Glu Val Ala Glu Glu Ile Ala Arg Leu Glu
158              245                 250                 255
159 Ala Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg
160              260                 265                 270
161 Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Gly Leu Pro Ala Ile
162          275                 280                 285
163 Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu
164      290                 295                 300
165 Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln Tyr
166 305                 310                 315                 320
167 Arg Glu Leu Thr Lys Leu Lys Ser Thr Tyr Ile Asp Pro Leu Pro Asp
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169 Leu Ile His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr
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171 Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn
172              355              360              365
173 Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Ile
174      370              375              380
175 Ala Glu Glu Gly Trp Leu Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu
176 385              390              395              400
177 Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val
178              405              410              415
179 Phe Gln Glu Gly Arg Asp Ile His Thr Glu Thr Ala Ser Trp Met Phe
180              420              425              430
181 Gly Val Pro Arg Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys
182              435              440              445
183 Thr Ile Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser
184      450              455              460
185 Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Gln Ala Phe Ile Glu Arg
186 465              470              475              480
187 Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu
188              485              490              495
189 Glu Glu Gly Arg Arg Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg
190              500              505              510
191 Arg Tyr Val Pro Asp Leu Glu Ala Arg Val Lys Ser Val Arg Glu Ala
192              515              520              525
193 Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp
194              530              535              540
195 Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Glu Glu Met
196 545              550              555              560
197 Gly Ala Arg Met Leu Leu Gln Val His Asp Glu Leu Val Leu Glu Ala
198              565              570              575
199 Pro Lys Glu Arg Ala Glu Ala Val Ala Arg Leu Ala Lys Glu Val Met
200              580              585              590
201 Glu Gly Val Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Ile
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211 <212> TYPE: DNA
212 <213> ORGANISM: Artificial Sequence
214 <220> FEATURE:
215 <223> OTHER INFORMATION: Description of Artificial Sequence:fusion protein
216      Ssod7d/full-length Taq
218 <220> FEATURE:
219 <221> NAME/KEY: CDS
220 <222> LOCATION: (1)..(2763)
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RAW SEQUENCE LISTING   DATE: 05/06/2003
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226 gagggcggtg gcaagaccgg ccgtggtgcg gtaagcgaaa aggacgcgcc gaaggagctg 180
227 ctgcagatgc tggagaagca gaaaaagggc ggcggtgtca ctagtgggat gctgcccctc 240
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235 ctcctttccg accgcatcca cgtcctccac cccgagggt acctcatcac cccggcctgg 720
236 ctttgggaaa agtacggcct gaggcccgac cagtgggccg actaccgggc cctgaccggg 780
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